Boolean Network models make decisions about probable links using conditional statements. Displayed is a truth table with takes every occurrence and calculates possible combinations. The flow of the model changes based on how the truth table is set up. The truth table helps to determine which nodes will be active and which will not. From here, the model will be updated based on which sections are linked together by edges. If certain pathways are connected, a node will deactivate itself, causing all other that rely on it to also deactivate. This creates a looping cycle which shows how the Boolean network operates.

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A few possible applications of these methods are fields of study, such as cancer research, and signaling network research, and showing possible knockout effects. Another application is the ability to run simulations to determine new pathways, which will allow for research to become more detailed and sophisticated.

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The genetic modification of E. coli has a large impact on the medical field. In the past, researchers have been able to reproduce compounds with the same effects as insulin, opioids, and vaccines. This field also has an effect in biotechnology, where the modification of E. coli effects several other aspects that are not necessarily related to biology.

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Our research project is based on the work done by Bioengineers at Kyoto University. They modified the genetic material of E. Coli using genes from other bacteria and enzymes from two opium poppies to produce precursors to morphine.

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We modeled our graphs and data by reproducing the chemicals from the blue path for E. coli, which results in an opioid.

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In our program we modeled the Boolean network for E. coli, and ran a simulation using truth tables to determine the outcome. We used file input and output to make modeling the data easier, and allowed us the ability to save each type of graph and model we produced.

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Discuss the images, and how the pathways are linked maybe.

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Describe what is happening in the example text file.

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Describe our network.

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We created our program to produce the models of the E. coli with the use of generations.

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Discuss the resulting images.

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The possible improvements to this method would be to make the model more realistic by adding in more E. coli pathways. This would mean that we could integrate our model with other E. coli networks to… We could also allow for asynchronous updating, or kinetic parameter integration. A way to improve our specific model production method would be to implement our own functions for graphing instead of using libraries that are available through python. This would allow us to program the functions to handle specific events, such as the removal of sections of the graph, or changing the connectivity of the chemical compounds.